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RAW SEQUENCE LISTING  
PATENT APPLICATION US/09/320,713

DATE: 06/10/1999  
TIME: 11:19:01

Input Set: I320713.RAW

This Raw Listing contains the General Information  
Section and up to first 5 pages.

1 <110> APPLICANT: Reinhard Ebner  
2 Steven M. Ruben  
3 <120> TITLE OF INVENTION: INTERLEUKINS-21 AND 22  
4 <130> FILE REFERENCE: PF470  
5 <140> CURRENT APPLICATION NUMBER: US/09/320,713  
6 <141> CURRENT FILING DATE: 1999-05-27  
7 <150> EARLIER APPLICATION NUMBER: 60/087,340  
8 <151> EARLIER FILING DATE: 1998-05-29  
9 <150> EARLIER APPLICATION NUMBER: 60/099,805  
10 <151> EARLIER FILING DATE: 1998-09-10  
11 <150> EARLIER APPLICATION NUMBER: 60/131,965  
12 <151> EARLIER FILING DATE: 1999-04-30  
13 <160> NUMBER OF SEQ ID NOS: 32  
14 <170> SOFTWARE: PatentIn Ver. 2.0  
15 <210> SEQ ID NO 1  
16 <211> LENGTH: 705  
17 <212> TYPE: DNA  
18 <213> ORGANISM: Homo sapiens  
19 <220> FEATURE:  
20 <221> NAME/KEY: CDS  
21 <222> LOCATION: (2)..(262)  
22 <400> SEQUENCE: 1  
23 g gca cga gtg gac acg gat gag gac cgc tat cca cag aag ctg gcc ttc 49  
24 Ala Arg Val Asp Thr Asp Glu Asp Arg Tyr Pro Gln Lys Leu Ala Phe  
25 1 5 10 15  
26 gcc gag tgc ctg tgc aga ggc tgt atc gat gca cgg acg ggc cgc gag 97  
27 Ala Glu Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu  
28 20 25 30  
29 aca gct gcg ctc aac tcc gtg cgg ctg ctc cag agc ctg ctg gtg ctg 145  
30 Thr Ala Ala Leu Asn Ser Val Arg Leu Leu Gln Ser Leu Leu Val Leu  
31 35 40 45  
32 cgc cgc cgg ccc tgc tcc cgc gac ggc tcg ggg ctc ccc aca cct ggg 193  
33 Arg Arg Arg Pro Cys Ser Arg Asp Gly Ser Gly Leu Pro Thr Pro Gly  
34 50 55 60  
35 gcc ttt gcc ttc cac acc gag ttc atc cac gtc ccc gtc ggc tgc acc 241  
36 Ala Phe Ala Phe His Thr Glu Phe Ile His Val Pro Val Gly Cys Thr  
37 65 70 75 80  
38 tgc gtg ctg ccc cgt tca gtg tgaccgccaa ggccgtgggg cccttagact 292  
39 Cys Val Leu Pro Arg Ser Val  
40 85  
41 ggacacgtgt gctccccaga gggcaccccc tatttatgtg tatttattgt tatttatatg 352  
42 cctcccccaa cactaccctt ggggtctggg cattccccgt gtctggagga cagccccca 412  
43 ctgttctcct catctccagc ctcagtagtt gggggwtgaa ggagctcagc acctcttcca 472  
44 gcccttaaag ctgcagaaaa ggtgtcacac ggctgcctgt accttggytc cctgtcctgc 532

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45 tccccgcttc ccttacccta tcactggcct caggcccccg caggctgcct cttcccaacc 592  
46 tccttggaag tacccctgtt tcttaaacia ttattttaagt gtacgtgtat tattaaactg 652  
47 atgaacacaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 705

48 <210> SEQ ID NO 2

49 <211> LENGTH: 87

50 <212> TYPE: PRT

51 <213> ORGANISM: Homo sapiens

52 <400> SEQUENCE: 2

53 Ala Arg Val Asp Thr Asp Glu Asp Arg Tyr Pro Gln Lys Leu Ala Phe  
54 1 5 10 15  
55 Ala Glu Cys Leu Cys Arg Gly Cys Ile Asp Ala Arg Thr Gly Arg Glu  
56 20 25 30  
57 Thr Ala Ala Leu Asn Ser Val Arg Leu Leu Gln Ser Leu Leu Val Leu  
58 35 40 45  
59 Arg Arg Arg Pro Cys Ser Arg Asp Gly Ser Gly Leu Pro Thr Pro Gly  
60 50 55 60  
61 Ala Phe Ala Phe His Thr Glu Phe Ile His Val Pro Val Gly Cys Thr  
62 65 70 75 80  
63 Cys Val Leu Pro Arg Ser Val  
64 85

65 <210> SEQ ID NO 3

66 <211> LENGTH: 1642

67 <212> TYPE: DNA

68 <213> ORGANISM: Homo sapiens

69 <220> FEATURE:

70 <221> NAME/KEY: CDS

71 <222> LOCATION: (3)..(482)

72 <400> SEQUENCE: 3

73 gg aat tcg gca cga gct cgt gcc gtg ctc agt gcc ttc cac cac acg 47  
74 Asn Ser Ala Arg Ala Arg Ala Val Leu Ser Ala Phe His His Thr  
75 1 5 10 15  
76 ctg cag ctg ggg ccg cgt gag cag gcg cgc aac gcg agc tgc ccg gca 95  
77 Leu Gln Leu Gly Pro Arg Glu Gln Ala Arg Asn Ala Ser Cys Pro Ala  
78 20 25 30  
79 ggg ggc agg ccc gcc gac cgc cgc ttc cgg ccg ccc acc aac ctg cgc 143  
80 Gly Gly Arg Pro Ala Asp Arg Arg Phe Arg Pro Pro Thr Asn Leu Arg  
81 35 40 45  
82 agc gtg tcg ccc tgg gcc tac aga atc tcc tac gac ccg gcg agg tac 191  
83 Ser Val Ser Pro Trp Ala Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Tyr  
84 50 55 60  
85 ccc agg tac ctg cct gaa gcc tac tgc ctg tgc cgg ggc tgc ctg acc 239  
86 Pro Arg Tyr Leu Pro Glu Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr  
87 65 70 75  
88 ggg ctg ttc ggc gag gag gac gtg cgc ttc cgc agc gcc cct gtc tac 287  
89 Gly Leu Phe Gly Glu Glu Asp Val Arg Phe Arg Ser Ala Pro Val Tyr  
90 80 85 90 95  
91 atg ccc acc gtc gtc ctg cgc cgc acc ccc gcc tgc gcc ggc ggc cgt 335  
92 Met Pro Thr Val Val Leu Arg Arg Thr Pro Ala Cys Ala Gly Gly Arg  
93 100 105 110  
94 tcc gtc tac acc gag gcc tac gtc acc atc ccc gtg ggc tgc acc tgc 383

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95      Ser Val Tyr Thr Glu Ala Tyr Val Thr Ile Pro Val Gly Cys Thr Cys
96                115                      120                      125
97      gtc ccc gag ccg gag aag gac gca gac agc atc aac tcc agc atc gac   431
98      Val Pro Glu Pro Glu Lys Asp Ala Asp Ser Ile Asn Ser Ser Ile Asp
99                130                      135                      140
100     aaa cag ggc gcc aag ctg ctg ggc ccc aac gac gcg ccc gct ggc   479
101     Lys Gln Gly Ala Lys Leu Leu Leu Gly Pro Asn Asp Ala Pro Ala Gly
102                145                      150                      155
103     ccc tgaggccggt cctgccccgg gaggtctccc cggcccgcat cccgaggcgc   532
104     Pro
105     160
106     ccaagctgga gccgcctgga gggctcggtc ggcgacctct gaagagagtg caccgagcaa 592
107     accaagtgcc ggagcaccag cgccgccttt ccatggagac tcgtaagcag cttcatctga 652
108     cacgggcatc cctggcttgc ttttagctac aagcaagcag cgtggctgga agctgatggg 712
109     aaacgacctg gcacgggcat cctgtgtgcg gcccgcattg agggtttgga aaagtccacg 772
110     gaggtccctc gaggagcctc tcagatcggc tgctgcgggt gcagggcgtg actcacgctc 832
111     ggggtgcttg caaagagata gggacgcata tgctttttta agcaatctaa aaataataat 892
112     aagtatagcg actatatacc tactttttaa atcaactgtt ttgaatagag gcagagctat 952
113     tttatattat caaatgagag ctactctgtt acatttctta acatataaac atcgtttttt 1012
114     acttcttctg gtagaatttt ttaaagcata attggaatcc ttggataaat tttgtagctg 1072
115     gtacactctg gcctgggtct ctgaattcag cctgtcaccc atggctgact gatgaaatgg 1132
116     acacgtctca tctgacctac tcttccttcc actgaaggtc ttcacgggcc tccaggtgga 1192
117     ccaaagggat gcacaggcgg ctgcgcatgcc ccagggccag ctaagagttc caaagatctc 1252
118     agatttggtt ttagtcatga atacataaac agtctcaaac tcgcacaatt ttttccccct 1312
119     tttgaaagcc actggggcca atttgtggtt aagagggtgt gagataagaa gtggaacgtg 1372
120     acatctttgc cagttgtcag aagaatccaa gcagggtatt gcttagttgt aagggtctta 1432
121     ggatcaggct gaatatgagg acaaagtggg ccacgttagc atctgcagag atcaatctgg 1492
122     aggcttctgt ttctgcattc tgccacgaga gctaggtcct tgatcttttc tttagattga 1552
123     aagtctgtct ctgaacacaa ttatttgtaa aagttagtag ttctttttta aatcattaaa 1612
124     agaggcttgc tgaaaaaaaa aaaaaaaaaa   1642
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126     <211> LENGTH: 160
127     <212> TYPE: PRT
128     <213> ORGANISM: Homo sapiens
129     <400> SEQUENCE: 4
130     Asn Ser Ala Arg Ala Arg Ala Val Leu Ser Ala Phe His His Thr Leu
131           1             5             10             15
132     Gln Leu Gly Pro Arg Glu Gln Ala Arg Asn Ala Ser Cys Pro Ala Gly
133           20             25             30
134     Gly Arg Pro Ala Asp Arg Arg Phe Arg Pro Pro Thr Asn Leu Arg Ser
135           35             40             45
136     Val Ser Pro Trp Ala Tyr Arg Ile Ser Tyr Asp Pro Ala Arg Tyr Pro
137           50             55             60
138     Arg Tyr Leu Pro Glu Ala Tyr Cys Leu Cys Arg Gly Cys Leu Thr Gly
139           65             70             75             80
140     Leu Phe Gly Glu Glu Asp Val Arg Phe Arg Ser Ala Pro Val Tyr Met
141           85             90             95
142     Pro Thr Val Val Leu Arg Arg Thr Pro Ala Cys Ala Gly Gly Arg Ser
143           100            105            110
144     Val Tyr Thr Glu Ala Tyr Val Thr Ile Pro Val Gly Cys Thr Cys Val

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145          115          120          125
146      Pro Glu Pro Glu Lys Asp Ala Asp Ser Ile Asn Ser Ser Ile Asp Lys
147          130          135          140
148      Gln Gly Ala Lys Leu Leu Leu Gly Pro Asn Asp Ala Pro Ala Gly Pro
149      145          150          155          160
150 <210> SEQ ID NO 5
151 <211> LENGTH: 155
152 <212> TYPE: PRT
153 <213> ORGANISM: Homo sapiens
154 <400> SEQUENCE: 5
155      Met Thr Pro Gly Lys Thr Ser Leu Val Ser Leu Leu Leu Leu Leu Ser
156          1          5          10          15
157      Leu Glu Ala Ile Val Lys Ala Gly Ile Thr Ile Pro Arg Asn Pro Gly
158          20          25          30
159      Cys Pro Asn Ser Glu Asp Lys Asn Phe Pro Arg Thr Val Met Val Asn
160          35          40          45
161      Leu Asn Ile His Asn Arg Asn Thr Asn Thr Asn Pro Lys Arg Ser Ser
162          50          55          60
163      Asp Tyr Tyr Asn Arg Ser Thr Ser Pro Trp Asn Leu His Arg Asn Glu
164          65          70          75          80
165      Asp Pro Glu Arg Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg His
166          85          90          95
167      Leu Gly Cys Ile Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser
168          100          105          110
169      Val Pro Ile Gln Gln Glu Ile Leu Val Leu Arg Arg Glu Pro Pro His
170          115          120          125
171      Cys Pro Asn Ser Phe Arg Leu Glu Lys Ile Leu Val Ser Val Gly Cys
172          130          135          140
173      Thr Cys Val Thr Pro Ile Val His His Val Ala
174      145          150          155
175 <210> SEQ ID NO 6
176 <211> LENGTH: 158
177 <212> TYPE: PRT
178 <213> ORGANISM: Mus musculus
179 <400> SEQUENCE: 6
180      Met Ser Pro Gly Arg Ala Ser Ser Val Ser Leu Met Leu Leu Leu Leu
181          1          5          10          15
182      Leu Ser Leu Ala Ala Thr Val Lys Ala Ala Ala Ile Ile Pro Gln Ser
183          20          25          30
184      Ser Ala Cys Pro Asn Thr Glu Ala Lys Asp Phe Leu Gln Asn Val Lys
185          35          40          45
186      Val Asn Leu Lys Val Phe Asn Ser Leu Gly Ala Lys Val Ser Ser Arg
187          50          55          60
188      Arg Pro Ser Asp Tyr Leu Asn Arg Ser Thr Ser Pro Trp Thr Leu His
189          65          70          75          80
190      Arg Asn Glu Asp Pro Asp Arg Tyr Pro Ser Val Ile Trp Glu Ala Gln
191          85          90          95
192      Cys Arg His Gln Arg Cys Val Asn Ala Glu Gly Lys Leu Asp His His
193          100          105          110
194      Met Asn Ser Val Leu Ile Gln Gln Glu Ile Leu Val Leu Lys Arg Glu

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195          115          120          125
196 Pro Glu Ser Cys Pro Phe Thr Phe Arg Val Glu Lys Met Leu Val Gly
197          130          135          140
198 Val Gly Cys Thr Cys Val Ala Ser Ile Val Arg Gln Ala Ala
199          145          150          155
200 <210> SEQ ID NO 7
201 <211> LENGTH: 151
202 <212> TYPE: PRT
203 <213> ORGANISM: Homo sapiens
204 <400> SEQUENCE: 7
205 Met Thr Phe Arg Met Thr Ser Leu Val Leu Leu Leu Leu Leu Ser Ile
206      1          5          10          15
207 Asp Cys Ile Val Lys Ser Glu Ile Thr Ser Ala Gln Thr Pro Arg Cys
208          20          25          30
209 Leu Ala Ala Asn Asn Ser Phe Pro Arg Ser Val Met Val Thr Leu Ser
210          35          40          45
211 Ile Arg Asn Trp Asn Thr Ser Ser Lys Arg Ala Ser Asp Tyr Tyr Asn
212          50          55          60
213 Arg Ser Thr Ser Pro Trp Thr Leu His Arg Asn Glu Asp Gln Asp Arg
214          65          70          75          80
215 Tyr Pro Ser Val Ile Trp Glu Ala Lys Cys Arg Tyr Leu Gly Cys Val
216          85          90          95
217 Asn Ala Asp Gly Asn Val Asp Tyr His Met Asn Ser Val Pro Ile Gln
218          100          105          110
219 Gln Glu Ile Leu Val Val Arg Lys Gly His Gln Pro Cys Pro Asn Ser
220          115          120          125
221 Phe Arg Leu Glu Lys Met Leu Val Thr Val Gly Cys Thr Cys Val Thr
222          130          135          140
223 Pro Ile Val His Asn Val Asp
224          145          150
225 <210> SEQ ID NO 8
226 <211> LENGTH: 180
227 <212> TYPE: PRT
228 <213> ORGANISM: Homo sapiens
229 <400> SEQUENCE: 8
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231      1          5          10          15
232 Leu Gly Leu Gly Gln Pro Arg Ser Pro Lys Ser Lys Arg Lys Gly Gln
233          20          25          30
234 Gly Arg Pro Gly Pro Leu Ala Pro Gly Pro His Gln Val Pro Leu Asp
235          35          40          45
236 Leu Val Ser Arg Met Lys Pro Tyr Ala Arg Met Glu Glu Tyr Glu Arg
237          50          55          60
238 Asn Ile Glu Glu Met Val Ala Gln Leu Arg Asn Ser Ser Glu Leu Ala
239          65          70          75          80
240 Gln Arg Lys Cys Glu Val Asn Leu Gln Leu Trp Met Ser Asn Lys Arg
241          85          90          95
242 Ser Leu Ser Pro Trp Gly Tyr Ser Ile Asn His Asp Pro Ser Arg Ile
243          100          105          110
244 Pro Val Asp Leu Pro Glu Ala Arg Cys Leu Cys Leu Gly Cys Val Asn

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> <223> fields of each sequence which presents at least one n or Xaa.

Input Set: I320713.RAW

Line Error/Warning

Original Text

Line	Error/Warning	Original Text
305	W "N" or "Xaa" used: Feature required	Trp Ser Xaa Trp Ser
432	W "N" or "Xaa" used: Feature required	naattcggca naggngaaa cgaccggca ngcgatnc
433	W "N" or "Xaa" used: Feature required	gtttggaaaa gttcacgng gtccttgag gacctgcg
434	W "N" or "Xaa" used: Feature required	aaggcgtgga ctaccgctg ggtgcttgcc aaanagga
436	W "N" or "Xaa" used: Feature required	ttgaatagag gcagagctta ttttatatta tccaaatg
437	W "N" or "Xaa" used: Feature required	ctttaaacat tttaaacatn gnttttttna cttcttnc
438	W "N" or "Xaa" used: Feature required	cnaattggg a
576	W "N" or "Xaa" used: Feature required	aattcggcag agccagnccg gagaaggacg cagacagc
577	W "N" or "Xaa" used: Feature required	agggcgccaa gctcctgctg ggccccaacg acgcgcc
578	W "N" or "Xaa" used: Feature required	ctgccccggg aggtctcccc ggncccgcat cccgaggc
579	W "N" or "Xaa" used: Feature required	ggnttcggtc ggcgactctg aagagagtnc accgagca
580	W "N" or "Xaa" used: Feature required	gncgnctttt ncatggagat tcgtaagcan ttttcatt
581	W "N" or "Xaa" used: Feature required	tttttagtta caagcaagca nntggnttga agtnngtg
582	W "N" or "Xaa" used: Feature required	tgtnttnggg gccntntgga gggttttgga aaatttna
583	W "N" or "Xaa" used: Feature required	anattggntt ttttaggggt tnaagggttn ntttaactt
584	W "N" or "Xaa" used: Feature required	ggattntttt tnaagatt
619	W "N" or "Xaa" used: Feature required	gttcagagac agactttcaa tctaaagaaa agatcaag
620	W "N" or "Xaa" used: Feature required	gcagaaacag aagccnccag atnganctcn gcagatgc
642	W "N" or "Xaa" used: Feature required	ggcagagcca agtcctgct ggngcccaa cgacgcgc
644	W "N" or "Xaa" used: Feature required	gggcttcggt ncggcgaacc tctgaaagag aagtgcc
645	W "N" or "Xaa" used: Feature required	gcaccagngc cgcctttcca tggagactcg taagcagc
772	W "N" or "Xaa" used: Feature required	agagcctgac tggtgctgcg ccgcccggcc tgactacc
773	W "N" or "Xaa" used: Feature required	cccacacctg ggncctttg acctccaca ccgnagtt
774	W "N" or "Xaa" used: Feature required	gctgtcacct gacgtgctgn ccccgtttac agtgtgna
775	W "N" or "Xaa" used: Feature required	ccctnagtac tggnacacgt gtgatacccc ag